

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/980,862B
Source: IFW/6
Date Processed by STIC: 6/9/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/09/2005

PATENT APPLICATION: US/09/980,862B

TIME: 15:29:29

Input Set : A:\29029101.app

Output Set: N:\CRF4\06092005\I980862B.raw

3 <110> APPLICANT: SCHLEHUBER, STEFFEN
 5 <120> TITLE OF INVENTION: MUTEINS OF THE BILIN-BINDING PROTEIN
 7 <130> FILE REFERENCE: 029029-0101
 9 <140> CURRENT APPLICATION NUMBER: 09/980,862B
 10 <141> CURRENT FILING DATE: 2002-02-27
 12 <150> PRIOR APPLICATION NUMBER: PCT/DE00/01873
 13 <151> PRIOR FILING DATE: 2000-06-08
 15 <150> PRIOR APPLICATION NUMBER: DE 199 26 068.0
 16 <151> PRIOR FILING DATE: 1999-06-08
 18 <160> NUMBER OF SEQ ID NOS: 29
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1219
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 29 pBBP20 nucleic acid sequence
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (22)..(1209)
 35 <220> FEATURE:
 36 <221> NAME/KEY: sig_peptide
 37 <222> LOCATION: (22)..(84)
 39 <220> FEATURE:
 40 <221> NAME/KEY: mat_peptide
 41 <222> LOCATION: (85)..(1209)
 42 <223> OTHER INFORMATION: fusion protein of bilin-binding protein, Strep-tag II
 43 and fragment of phage coat protein pIII
 45 <220> FEATURE:
 46 <221> NAME/KEY: misc_feature
 47 <222> LOCATION: (85)..(606)
 48 <223> OTHER INFORMATION: mature bilin-binding protein
 50 <220> FEATURE:
 51 <221> NAME/KEY: misc_feature
 52 <222> LOCATION: (607)..(636)
 53 <223> OTHER INFORMATION: Strep-tag II-affinity tag
 55 <220> FEATURE:
 56 <221> NAME/KEY: misc_feature
 57 <222> LOCATION: (637)..(639)
 58 <223> OTHER INFORMATION: amber stop codon
 60 <220> FEATURE:
 61 <221> NAME/KEY: misc_feature

(pg.6)

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62 <222> LOCATION: (640)..(1209)
63 <223> OTHER INFORMATION: amino acids 217-406 of coat protein pIII
65 <400> SEQUENCE: 1
66 tctagttaac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg 51
67                               Met Lys Lys Thr Ala Ile Ala Ile Ala Val
68                               -20                               -15
70 gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac 99
71 Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
72   -10                               -5                               -1   1   5
74 ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag 147
75 Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
76                               10                               15                               20
78 tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag 195
79 Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu
80                               25                               30                               35
82 aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt 243
83 Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
84   40                               45                               50
86 gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att 291
87 Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile
88   55                               60                               65
90 gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac 339
91 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
92 70                               75                               80                               85
94 cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta 387
95 His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val
96                               90                               95                               100
98 ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac 435
99 Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr
100                               105                               110                               115
102 gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga 483
103 Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg
104                               120                               125                               130
106 agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt 531
107 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu
108   135                               140                               145
110 atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc 579
111 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
112 150                               155                               160                               165
114 tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag 627
115 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln
116                               170                               175                               180
118 ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc 675
119 Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
120                               185                               190                               195
122 tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct 723
123 Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
124   200                               205                               210
126 gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat 771

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127 Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
128      215      220      225
130 gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat 819
131 Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp
132 230      235      240      245
134 gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct 867
135 Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala
136      250      255      260
138 act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc 915
139 Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
140      265      270      275
142 ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc 963
143 Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser
144      280      285      290
146 caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat 1011
147 Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn
148      295      300      305
150 ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct 1059
151 Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro
152 310      315      320      325
154 ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac 1107
155 Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
156      330      335      340
158 aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc 1155
159 Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
160      345      350      355
162 acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag 1203
163 Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
164      360      365      370
166 gag tct taataagctt 1219
167 Glu Ser
168      375
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 64
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
179 <220> FEATURE:
180 <221> NAME/KEY: modified_base
181 <222> LOCATION: (35)..(36)
182 <223> OTHER INFORMATION: a, t, c, g, other or unknown
184 <220> FEATURE:
185 <221> NAME/KEY: modified_base
186 <222> LOCATION: (38)
187 <223> OTHER INFORMATION: a, t, c, g, other or unknown
189 <220> FEATURE:
190 <221> NAME/KEY: modified_base
191 <222> LOCATION: (41)..(42)

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192 <223> OTHER INFORMATION: a, t, c, g, other or unknown
194 <220> FEATURE:
195 <221> NAME/KEY: modified_base
196 <222> LOCATION: (44)..(45)
197 <223> OTHER INFORMATION: a, t, c, g, other or unknown
199 <400> SEQUENCE: 2
W--> 200 ccatggtaaa tgggtgggaag tcgccaaata ccccnknms nnsnkaagt acggaaagt 60
      201 cgga                                         64
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 71
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
212 <220> FEATURE:
213 <221> NAME/KEY: modified_base
214 <222> LOCATION: (19)..(20)
215 <223> OTHER INFORMATION: a, t, c, g, other or unknown
217 <220> FEATURE:
218 <221> NAME/KEY: modified_base
219 <222> LOCATION: (46)..(47)
220 <223> OTHER INFORMATION: a, t, c, g, other or unknown
222 <220> FEATURE:
223 <221> NAME/KEY: modified_base
224 <222> LOCATION: (52)..(53)
225 <223> OTHER INFORMATION: a, t, c, g, other or unknown
227 <400> SEQUENCE: 3
W--> 228 gggtaggcgg taccttcsnn aaagtattcc ttgccgtgga ttacmngta snncgaaact 60
      229 ttgacactct t                                         71
232 <210> SEQ ID NO: 4
233 <211> LENGTH: 74
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
240 <220> FEATURE:
241 <221> NAME/KEY: modified_base
242 <222> LOCATION: (27)..(28)
243 <223> OTHER INFORMATION: a, t, c, g, other or unknown
245 <220> FEATURE:
246 <221> NAME/KEY: modified_base
247 <222> LOCATION: (33)..(34)
248 <223> OTHER INFORMATION: a, t, c, g, other or unknown
250 <220> FEATURE:
251 <221> NAME/KEY: modified_base
252 <222> LOCATION: (42)..(43)
253 <223> OTHER INFORMATION: a, t, c, g, other or unknown
255 <220> FEATURE:
256 <221> NAME/KEY: modified_base

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Input Set : A:\29029101.app

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257 <222> LOCATION: (54)..(55)
258 <223> OTHER INFORMATION: a, t, c, g, other or unknown
260 <400> SEQUENCE: 4
W--> 261 ccaagattgg aaagatctac cacagcnnsa ctnnkggagg tnsaccvvs gagnnkgatat 60
      262 tcaacgtact ctcc 74
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 78
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
273 <220> FEATURE:
274 <221> NAME/KEY: modified_base
275 <222> LOCATION: (20)..(21)
276 <223> OTHER INFORMATION: a, t, c, g, other or unknown
278 <220> FEATURE:
279 <221> NAME/KEY: modified_base
280 <222> LOCATION: (26)..(27)
281 <223> OTHER INFORMATION: a, t, c, g, other or unknown
283 <220> FEATURE:
284 <221> NAME/KEY: modified_base
285 <222> LOCATION: (53)..(54)
286 <223> OTHER INFORMATION: a, t, c, g, other or unknown
288 <220> FEATURE:
289 <221> NAME/KEY: modified_base
290 <222> LOCATION: (59)..(60)
291 <223> OTHER INFORMATION: a, t, c, g, other or unknown
293 <400> SEQUENCE: 5
W--> 294 tctggagagc acccagacmn ngtcsnngtg tcccttcttg tcctcgtcgt asnngcamnn 60
      295 gtatccgatg atgtagtt 78
298 <210> SEQ ID NO: 6
299 <211> LENGTH: 36
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
306 <400> SEQUENCE: 6
307 cttcgactgg tccagtagc atggtaaag gtaggga 36
310 <210> SEQ ID NO: 7
311 <211> LENGTH: 37
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
318 <400> SEQUENCE: 7
319 caccagtaag gaccatgctt ctggagagca cccagac 37
322 <210> SEQ ID NO: 8
323 <211> LENGTH: 46
324 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/980,862B

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Input Set : A:\29029101.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 35, 36, 38, 41, 42, 44, 45
Seq#:3; N Pos. 19, 20, 46, 47, 52, 53
Seq#:4; N Pos. 27, 28, 38, 39, 42, 48, 52, 53
Seq#:5; N Pos. 20, 21, 26, 27, 53, 54, 59, 60
Seq#:13; N Pos. 29, 30, 38, 39, 47, 48, 50, 51, 53, 54, 56, 57

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:16; Line(s) 906

VERIFICATION SUMMARY

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Input Set : A:\29029101.app

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L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:636 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 14, CDS LOCATION:22..1209
L:874 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16